

Conseiller.ST25  
SUBSTITUTE SEQUENCE LISTING

<110> Conseiller, Emmanuel  
Debussche, Laurent  
Gallagher, William

<120> Polypeptide (MBP1) Capable Of Interacting With Oncogenic Mutants Of The P53 Protein

<130> ST98033

<140> 09/829,936

<141> 2001-04-11

<150> FR9812754  
<151> 1998-10-12

<160> 35

<170> PatentIn version 3.3

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>  
<223> oligonucleotide 5'-1(p53)

<400> 1  
agatctgtat ggaggagccg cag

23

<210> 2

<211> 29

<212> DNA

<213> Artificial Sequence

<220>  
<223> oligonucleotide 3' -393 (p53)

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<400> 2  
agatctcatc agtctgagtc aggcccttc

29

<210> 3

<211> 15

<212> DNA

<213> Artificial Sequence

<220>  
<223> oligonucleotide H175 3'

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ggggcagtgc ctcac

15

<210> 4

<211> 15

<212> DNA

<213> Artificial Sequence

<220>  
<223> oligonucleotide w248 3'

<400> 4  
gggcctccag ttcac

15

<210> 5

<211> 15

<212> DNA

<213> Artificial Sequence

<220>  
<223> oligonucleotide H273 3'

<400> 5  
acaaacatgc acctc

15

<210> 6

<211> 15

<212> DNA

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<213> Artificial Sequence

<220>

<223> oligonucleotide G281 3'

<400> 6

gcgccggcct ctccc

15

<210> 7

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5'-73

<400> 7

agatctgtgt ggcccctgca cca

23

<210> 8

<211> 1021

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 C-term fragment

<220>

<221> CDS

<222> (1)..(885)

<400> 8

tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg gac  
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
1 5 10 15

48

ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg  
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

96

ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct  
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

144

aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca  
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

192

tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt  
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys

240

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65	70					75					80					
aac Asn	cag Gln	ggc Gly	tat Tyr	gag Glu 85	ctg Leu	cac His	cgg Arg	gat Asp	ggc Gly 90	ttc Phe	tcc Ser	tgc Cys	agc Ser	gat Asp 95	atc Ile	288
gat Asp	gag Glu	tgc Cys	ggc Gly 100	tac Tyr	tcc Ser	agt Ser	tac Tyr	ctc Leu 105	tgc Cys	cag Gln	tac Tyr	cgc Arg	tgt Cys 110	gtc Val	aac Asn	336
gag Glu	cca Pro	ggc Gly 115	cga Arg	ttc Phe	tcc Ser	tgt Cys	cac His 120	tgc Cys	cca Pro	caa Gln	ggc Gly 125	tac Tyr	cag Gln	ctg Leu	ctg Leu	384
gct Ala	aca Thr 130	agg Arg	ctc Leu	tgc Cys	caa Gln	gat Asp 135	att Ile	gac Asp	gag Glu	tgt Cys	gaa Glu 140	aca Thr	ggt Gly	gca Ala	cac His	432
caa Gln 145	tgt Cys	tct Ser	gag Glu	gcc Ala	caa Gln 150	acc Thr	tgt Cys	gtc Val	aac Asn	ttc Phe 155	cat His	ggg Gly	ggt Gly	tac Tyr	cgc Arg 160	480
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aac Asn	cgc Arg	tgc Cys	ctc Leu 180	tgc Cys	cct Pro	gcc Ala	tcc Ser	aat Asn 185	ccc Pro	ctt Leu	tgt Cys	cga Arg	gag Glu 190	cag Gln	cct Pro	576
tca Ser	tcc Ser	att Ile 195	gtg Val	cac His	cgc Arg	tac Tyr	atg Met 200	agc Ser	atc Ile	acc Thr	tca Ser	gag Glu 205	cga Arg	agt Ser	gtg Val	624
cct Pro 210	gct Ala	gac Asp	gtg Val	ttt Phe	cag Gln	atc Ile 215	cag Gln	gca Ala	acc Thr	tct Ser	gtc Val 220	tac Tyr	cct Pro	ggt Gly	gcc Ala	672
tac Tyr 225	aat Asn	gcc Ala	ttt Phe	cag Gln	atc Ile 230	cgt Arg	tct Ser	gga Gly	aac Asn	aca Thr 235	cag Gln	ggg Gly	gac Asp	ttc Phe	tac Tyr 240	720
att Ile	agg Arg	caa Gln	atc Ile	aac Asn 245	aat Asn	gtc Val	agc Ser	gcc Ala	atg Met 250	ctg Leu	gtc Val	ctc Leu	gcc Ala	agg Arg 255	cca Pro	768
gtg Val	acg Thr	gga Gly	ccc Pro 260	cgg Arg	gag Glu	tac Tyr	gtg Val	ctg Leu 265	gac Asp	ctg Leu	gag Glu	atg Met	gtc Val 270	acc Thr	atg Met	816
aat Asn	tcc Ser	ctt Leu 275	atg Met	agc Ser	tac Tyr	cgg Arg	gcc Ala 280	agc Ser	tct Ser	gta Val	ctg Leu	aga Arg 285	ctc Leu	acg Thr	gtc Val	864
ttt Phe 290	gtg Val	gga Gly	gcc Ala	tat Tyr	acc Thr	ttc Phe 295	tgaagaccct	cagggaagg	ccatgtggg							915
gccccttccc	cctcccatag	cttaagcagc	cccgggggcc	tagggatgac	cgttctgctt											975
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<210> 9

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine MBP1 C-term fragment

<400> 9

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His  
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp  
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
180 185 190

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Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val  
 195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
 210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr  
 225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
 245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
 260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
 275 280 285

Phe Val Gly Ala Tyr Thr Phe  
 290 295

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide c-myc 5'

<400> 10

gatccatgga gcagaagctg atctccgagg aggacctga

39

<210> 11

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide c-myc 3'

<400> 11

gatctcaggt cctcctcgga gatcagcttc tgctccatg

39

<210> 12

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<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' MCS oligonucleotide

<400> 12

gatctcggtc gacctgcatg caattcccgg gtgcggccgc gagct

45

<210> 13

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' MCS oligonucleotide

<400> 13

cgcggccgca cccgggaatt gcatgcaggt cgaccga

37

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' mMBP1

<400> 14

cggtactggc agaggtaact gg

22

<210> 15

<211> 1513

<212> DNA

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<220>

<221> CDS

<222> (49)..(1377)

# Conseiller.ST25

<400> 15  
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Met Leu Pro  
1

ttt gcc tcc tgc ctc ccc ggg tct ttg ctg ctc tgg gcg ttt ctg ctg 105  
Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu  
5 10 15

ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc 153  
Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu Pro Asp Ser  
20 25 30 35

tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac 201  
Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His  
40 45 50

tgc cgg gat gtc aac gag tgc ctg acc atc ccg gag gct tgc aag ggt 249  
Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly  
55 60 65

gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc 297  
Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys Leu Pro Arg  
70 75 80

tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca 345  
Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro  
85 90 95

gcg gcc cat gct caa caa cca aac cct tgc ccg cag ggc tac gag cct 393  
Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly Tyr Glu Pro  
100 105 110 115

gat gaa cag gag agc tgt gtg gat gtg gac gag tgt acc cag gct ttg 441  
Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr Gln Ala Leu  
120 125 130

cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac 489  
His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro Gly Ser Tyr  
135 140 145

cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg 537  
Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val  
150 155 160

gac ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac 585  
Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn  
165 170 175

ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga 633  
Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly  
180 185 190 195

cct aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc 681  
Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala  
200 205 210

cca tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc 729  
Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg  
215 220 225



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tgt aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat	777
Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp	
230 235 240	
atc gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc	825
Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val	
245 250 255	
aac gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg	873
Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu	
260 265 270 275	
ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca	921
Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala	
280 285 290	
cac caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac	969
His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr	
295 300 305	
cgc tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca	1017
Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser	
310 315 320	
gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag	1065
Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln	
325 330 335	
cct tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt	1113
Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser	
340 345 350 355	
gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt	1161
Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly	
360 365 370	
gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc	1209
Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe	
375 380 385	
tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg	1257
Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg	
390 395 400	
cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc	1305
Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr	
405 410 415	
atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg	1353
Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr	
420 425 430 435	
gtc ttt gtg gga gcc tat acc ttc tgaagaccct caggggaaggg ccatgtgggg	1407
Val Phe Val Gly Ala Tyr Thr Phe	
440	
gccccctccc cctcccatag cttaagcagc cccggggggcc tagggatgac cgttctgctt	1467
aaaggaacta tgatgtgaag gacaataaag ggagaaaagaa ggaaaa	1513

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<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<400> 16

Met Leu Pro Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
1 5 10 15

Phe Leu Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu  
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp  
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro  
85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly  
100 105 110

Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr  
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
195 200 205

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Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
210 215 220

Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr  
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
275 280 285

Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val  
305 310 315 320

Gln Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser  
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln  
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val  
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
435 440

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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' hMBP1

<400> 17

ctccgctccg aggtgatggt c

21

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5' hMBP1

<400> 18

tgtagctact ccagctacct c

21

<210> 19

<211> 1122

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

<400> 19

aagccagccg agccgccaga gccgcggggc gcggggggtgt cgcggggcca accccaggat 60

gctcccctgc gcctcctgcc taccggggtc tctactgctc tgggcgctgc tactgttgct 120

cttgggatca gcttctcctc aggattctga agagcccgac agctacacgg aatgcacaga 180

tggctatgag tgggaccag acagccagca ctgccgggat gtcaacgagt gtctgaccat 240

ccctgaggcc tgcaagggg aaatgaagt catcaaccac tacgggggct acttgtgcct 300

gccccgctcc gctgccgtca tcaacgacct acacggcgag ggacccccgc caccagtgcc 360

tcccgtcaa caccccaacc cctgcccacc aggctatgag cccgacgac aggacagctg 420

tgtggatgtg gacgagtgtg cccaggccct gcacgactgt cgccccagcc aggactgcca 480

taacttgctt ggctcctatc agtgcacctg ccctgatggt taccgcaaga tcgggcccga 540

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gtgtgtggac atagacgagt gccgctaccg ctactgccag caccgctgcg tgaacctgcc	600
tggctccttc cgctgccagt gcgagccggg cttccagctg gggcctaaca accgctcctg	660
tgttgatgtg aacgagtgtg acatgggggc cccatgagag cagcgtgct tcaactccta	720
tgggaccttc ctgtgtcgct gccaccaggg ctatgagctg catcgggatg gcttctcctg	780
cagtgatatt gatgagtgtg gctactccag ctacctctgt cagtaccgct gcgtcaacga	840
gccaggccgt ttctcctgcc actgcccaca gggttaccag ctgctggcca cacgcctctg	900
ccaagacatt gatgagtgtg agtctggtgc gcaccagtgc tccgaggccc aaacctgtgt	960
caacttccat gggggctacc gctgcgtgga caccaaccgc tgcgtggagc cctacatcca	1020
ggctctctgag aaccgctgtc tctgcccggc ctccaaccct ctatgtcgag agcagccttc	1080
atccattgtg caccgctaca tgaccatcac ctcggagcgg ag	1122

<210> 20

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

<400> 20

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tgccactgcc cacagggtta ccagctgctg gccacacgcc tctgccaaga cattgatgag	120
tgtgagtctg gtgcgaccca gtgctccgag gcccaaacct gtgtcaactt ccatgggggc	180
taccgctgag tggacaccaa ccgctgcgtg gagccctaca tccaggcttc tgagaaccgc	240
tgtctctgcc cggcctccaa ccctctatgt cgagagcagc cttcatccat tgtgcaccgc	300
tacatgacca tcacctcgga gcggagcgtg cccgctgacg tgttccagat ccaggcgacc	360
tccgtctacc ccggtgccta caatgccttt cagatccgtg ctggaaactc gcagggggac	420
ttttacatta ggcaaatcaa caacgtcagc gccatgctgg tcctcgcccc gccggtgacg	480
ggcccccgag agtacgtgct ggacctggag atggtcacca tgaattccct catgagctac	540
cgggccagct ctgtactgag gtcaccgtc tttgtagggg cctacacctt ctgaggagca	600
ggagggagcc accctccctg cagctaccct agctgaggag cctgttgtga ggggcagaat	660
gagaaaggca ataaaggag aaag	684

<210> 21

<211> 1480

# Conseiller.ST25

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<220>

<221> CDS

<222> (59)..(1387)

<400> 21

aagccagccg agccgccaga gccgcgggcc gcgggggtgt cgcgggccca accccagg 58

atg ctc ccc tgc gcc tcc tgc cta ccc ggg tct cta ctg ctc tgg gcg 106  
Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
1 5 10 15

ctg cta ctg ttg ctc ttg gga tca gct tct cct cag gat tct gaa gag 154  
Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu  
20 25 30

ccc gac agc tac acg gaa tgc aca gat ggc tat gag tgg gac cca gac 202  
Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp  
35 40 45

agc cag cac tgc cgg gat gtc aac gag tgt ctg acc atc cct gag gcc 250  
Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

tgc aag ggg gaa atg aag tgc atc aac cac tac ggg ggc tac ttg tgc 298  
Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

ctg ccc cgc tcc gct gcc gtc atc aac gac cta cac ggc gag gga ccc 346  
Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro  
85 90 95

ccg cca cca gtg cct ccc gct caa cac ccc aac ccc tgc cca cca ggc 394  
Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly  
100 105 110

tat gag ccc gac gat cag gac agc tgt gtg gat gtg gac gag tgt gcc 442  
Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala  
115 120 125

cag gcc ctg cac gac tgt cgc ccc agc cag gac tgc cat aac ttg cct 490  
Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140

ggc tcc tat cag tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc 538  
Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160

gag tgt gtg gac ata gac gag tgc cgc tac cgc tac tgc cag cac cgc 586  
Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175

tgc gtg aac ctg cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc 634  
Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

cag ctg ggg cct aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac 682

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Gln	Leu	Gly	Pro	Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	Asp	
		195					200					205				
atg	ggg	gcc	cca	tgc	gag	cag	cgc	tgc	ttc	aac	tcc	tat	ggg	acc	ttc	730
Met	Gly	Ala	Pro	Cys	Glu	Gln	Arg	Cys	Phe	Asn	Ser	Tyr	Gly	Thr	Phe	
	210					215					220					
ctg	tgt	cgc	tgc	cac	cag	ggc	tat	gag	ctg	cat	cgg	gat	ggc	ttc	tcc	778
Leu	Cys	Arg	Cys	His	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser	
225					230					235					240	
tgc	agt	gat	att	gat	gag	tgt	agc	tac	tcc	agc	tac	ctc	tgt	cag	tac	826
Cys	Ser	Asp	Ile	Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	
				245					250					255		
cgc	tgc	gtc	aac	gag	cca	ggc	cgt	ttc	tcc	tgc	cac	tgc	cca	cag	ggc	874
Arg	Cys	Val	Asn	Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	
			260					265					270			
tac	cag	ctg	ctg	gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag	922
Tyr	Gln	Leu	Leu	Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	
		275					280					285				
tct	ggt	gcg	cac	cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat	970
Ser	Gly	Ala	His	Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	
	290					295					300					
ggg	ggc	tac	cgc	tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc	1018
Gly	Gly	Tyr	Arg	Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	
305					310					315					320	
cag	gtc	tct	gag	aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt	1066
Gln	Val	Ser	Glu	Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	
				325					330					335		
cga	gag	cag	cct	tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg	1114
Arg	Glu	Gln	Pro	Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	
			340					345					350			
gag	cgg	agc	gtg	ccc	gct	gac	gtg	ttc	cag	atc	cag	gcg	acc	tcc	gtc	1162
Glu	Arg	Ser	Val	Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	
		355					360					365				
tac	ccc	ggt	gcc	tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag	1210
Tyr	Pro	Gly	Ala	Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	
	370					375					380					
ggg	gac	ttt	tac	att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc	1258
Gly	Asp	Phe	Tyr	Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	
385					390					395					400	
ctc	gcc	cgg	ccg	gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	1306
Leu	Ala	Arg	Pro	Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	
				405					410					415		
atg	gtc	acc	atg	aat	tcc	ctc	atg	agc	tac	cgg	gcc	agc	tct	gta	ctg	1354
Met	Val	Thr	Met	Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	
			420					425					430			
agg	ctc	acc	gtc	ttt	gta	ggg	gcc	tac	acc	ttc	tgaggagcag	gagggagcca				1407
Arg	Leu	Thr	Val	Phe	Val	Gly	Ala	Tyr	Thr	Phe						
		435					440									

Conseiller.ST25

ccctccctgc agctacccta gctgaggagc ctgttgtgag gggcagaatg agaaaggcaa 1467  
 taaagggaga aag 1480

<210> 22

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<400> 22

Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
 1 5 10 15

Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu  
 20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp  
 35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
 50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
 65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro  
 85 90 95

Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly  
 100 105 110

Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala  
 115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
 130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
 145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
 165 170 175



Conseiller.ST25  
Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
210 215 220

Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr  
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
275 280 285

Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile  
305 310 315 320

Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser  
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln  
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val  
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
420 425 430

Conseiller.ST25

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
435 440

<210> 23

<211> 817

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 cDNA (partial sequence)

<400> 23

gctgtggcag aaacccctga cttctgcccc ccacctccca gcctcaggat gctccctttt	60
gcctcctgcc tccccgggtc tttgctgctc tgggcgtttc tgctgttgct cttgggagca	120
gcgtcccccac aggatcccga ggagccggac agctacacgg aatgcacaga tggctatgag	180
tgggatgcag acagccagca ctgccgggat gtcaacgagt gcctgaccat cccggaggct	240
tgcaagggtg agatgaaatg catcaaccac tacggggggtt atttgtgtct gcctcgctct	300
gctgccgtca tcagtgatct ccatggtgaa ggacctccac cgccagcggc ccatgctcaa	360
caaccaaacc cttgcccgcg gggctacgag cctgatgaac aggagagctg tgtggatgtg	420
gacgagtgtg cccaggcttt gcatgactgt cgccctagtc aggactgcc taaccttcct	480
ggctcctacc agtgcacctg ccctgatggt taccgaaaaa ttggaccgga atgtgtggac	540
atagatgagt gtcgttaccg ctattgccag catcgatgtg tgaacctgcc gggctctttt	600
cgatgccagt gtgagccagg cttccagttg ggacctaa accgctcttg tgtggatgtg	660
aatgagtgtg acatgggagc cccatgtgag cagcgctgct tcaactccta tgggaccttc	720
ctgtgtcgct gtaaccaggg ctatgagctg caccgggatg gcttctcctg cagcgatatc	780
gatgagtgcg gctactccag ttacctctgc cagtacc	817

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-GAPDH oligonucleotide

<400> 24

cggagtcaac ggatttggtc gtat

Conseiller.ST25

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-GAPDH oligonucleotide

<400> 25

agccttctcc atggtggtga agac

24

<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-beta-actin oligonucleotide

<400> 26

cggttggcct tggggttcag ggggg

25

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-MBP1 oligonucleotide

<400> 27

gccctgatgg ttaccgcaag a

21

<210> 28

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense MBP1 oligonucleotide

# Conseiller.ST25

<400> 28  
agcccccatg gaagttgaca c 21

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-beta-actin oligonucleotide

<400> 29  
gtggggcgcc ccaggcacca 20

<210> 30

<211> 1358

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<220>

<221> CDS

<222> (1)..(885)

<400> 30  
tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc gag tgt gtg gac 48  
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
1 5 10 15

ata gac gag tgc cgc tac cgc tac tgc cag cac cgc tgc gtg aac ctg 96  
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc cag ctg ggg cct 144  
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac atg ggg gcc cca 192  
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgc 240  
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc tgc agt gat att 288  
His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95

gat gag tgt agc tac tcc agc tac ctc tgt cag tac cgc tgc gtc aac 336

Conseiller.ST25

Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	Arg	Cys	Val	Asn		
			100					105					110				
gag	cca	ggc	cgt	ttc	tcc	tgc	cac	tgc	cca	cag	ggt	tac	cag	ctg	ctg	384	
Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	Tyr	Gln	Leu	Leu		
		115					120					125					
gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag	tct	ggt	gcg	cac	432	
Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	Ser	Gly	Ala	His		
	130					135					140						
cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat	ggg	ggc	tac	cgc	480	
Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	Gly	Gly	Tyr	Arg		
145					150				155						160		
tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc	cag	gtc	tct	gag	528	
Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	Gln	Val	Ser	Glu		
				165					170					175			
aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt	cga	gag	cag	cct	576	
Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	Arg	Glu	Gln	Pro		
			180					185					190				
tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg	gag	cgg	agc	gtg	624	
Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	Glu	Arg	Ser	Val		
		195					200					205					
ccc	gct	gac	gtg	ttc	cag	atc	cag	gcg	acc	tcc	gtc	tac	ccc	ggt	gcc	672	
Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	Tyr	Pro	Gly	Ala		
	210					215					220						
tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag	ggg	gac	ttt	tac	720	
Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	Gly	Asp	Phe	Tyr		
225					230				235						240		
att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc	ctc	gcc	cgg	ccg	768	
Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	Leu	Ala	Arg	Pro		
				245					250					255			
gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	atg	gtc	acc	atg	816	
Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	Met	Val	Thr	Met		
			260					265					270				
aat	tcc	ctc	atg	agc	tac	cgg	gcc	agc	tct	gta	ctg	agg	ctc	acc	gtc	864	
Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	Arg	Leu	Thr	Val		
		275					280					285					
ttt	gta	ggg	gcc	tac	acc	ttc	tgaggagcag	gagggagcca	ccctccctgc							915	
Phe	Val	Gly	Ala	Tyr	Thr	Phe											
	290					295											
agctacccta	gctgaggagc	ctgttgtag	gggcagaatg	agaaaggcaa	taaagggaga											975	
aagaaagtcc	tggtggctga	ggtgggcggg	tcacactgca	ggaagcctca	ggctggggca											1035	
gggtggcact	tggggggggca	ggccaagtcc	acctaaatgg	gggtctctat	atgttcaggc											1095	
ccagggggccc	ccattgacag	gagctgggag	ctctgcacca	cgagcttcag	tcaccccag											1155	
aggagaggag	gtaacgagga	gggcggactc	caggccccgg	cccagagatt	tggacttggc											1215	
tggcttgtag	gggtcctaag	aaactccact	ctggacagcg	ccaggaggcc	ctgggttcca											1275	

Conseiller.ST25

ttcctaactc tgcctcaaac tgtacatttg gataagccct agtagttccc tgggcctgtt 1335  
 tttctataaa acgaggcaac tgg 1358

<210> 31

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<400> 31

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
 1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
 20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
 35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
 50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
 65 70 75 80

His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
 85 90 95

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
 100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
 115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His  
 130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
 145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu  
 165 170 175

# Conseiller.ST25

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
180 185 190

Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val  
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr  
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
275 280 285

Phe Val Gly Ala Tyr Thr Phe  
290 295

<210> 32

<211> 1663

<212> DNA

<213> Artificial Sequence

<220>

<223> murine fibulin 2 c-term fragment

<220>

<221> CDS

<222> (1)..(999)

<400> 32

gag ggc tct gaa tgt gtg gat gtg aat gag tgt gag aca ggt gtg cat	48
Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His	
1 5 10 15	

cgc tgt ggc gag ggc caa ctg tgc tat aac ctc cct gga tcc tac cgc	96
Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg	
20 25 30	

tgt gac tgc aag ccc ggc ttc cag agg gat gca ttc ggc agg act tgc	144
Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys	
35 40 45	

att gat gtg aac gaa tgc tgg gtc tcg ccg ggc cgc ctg tgc cag cac	192
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Conseiller.ST25

Ile	Asp	Val	Asn	Glu	Cys	Trp	Val	Ser	Pro	Gly	Arg	Leu	Cys	Gln	His	
50						55					60					
aca Thr 65	tgt Cys	gag Glu	aac Asn	aca Thr	ccg Pro 70	ggc Gly	tcc Ser	tac Tyr	cgc Arg	tgc Cys 75	tcc Ser	tgc Cys	gct Ala	gct Ala	ggc Gly 80	240
ttc Phe	ctt Leu	ttg Leu	gcc Ala	gca Ala 85	gat Asp	ggc Gly	aaa Lys	cat His	tgt Cys 90	gaa Glu	gat Asp	gtg Val	aac Asn	gag Glu 95	tgc Cys	288
gag Glu	act Thr	cgg Arg	cgc Arg 100	tgc Cys	agc Ser	cag Gln	gaa Glu	tgt Cys 105	gcc Ala	aac Asn	atc Ile	tat Tyr	ggc Gly 110	tcc Ser	tat Tyr	336
cag Gln	tgc Cys	tac Tyr 115	tgc Cys	cgt Arg	cag Gln	ggc Gly	tac Tyr 120	cag Gln	ctg Leu	gca Ala	gag Glu	gat Asp 125	ggg Gly	cat His	acc Thr	384
tgc Cys 130	aca Thr	gac Asp	atc Ile	gat Asp	gag Glu	tgt Cys 135	gca Ala	cag Gln	ggc Gly	gca Ala	ggc Gly 140	att Ile	ctc Leu	tgt Cys	acc Thr	432
ttc Phe 145	cgc Arg	tgt Cys	gtc Val	aac Asn	gtg Val 150	cct Pro	ggg Gly	agc Ser	tac Tyr	cag Gln 155	tgt Cys	gca Ala	tgc Cys	cca Pro	gag Glu 160	480
caa Gln	ggg Gly	tat Tyr	aca Thr	atg Met 165	atg Met	gcc Ala	aac Asn	ggg Gly	agg Arg 170	tcc Ser	tgc Cys	aag Lys	gac Asp	ctg Leu 175	gat Asp	528
gag Glu	tgt Cys	gca Ala	ctg Leu 180	ggc Gly	acc Thr	cac His	aac Asn	tgc Cys 185	tct Ser	gag Glu	gct Ala	gag Glu	acc Thr 190	tgc Cys	cac His	576
aat Asn	atc Ile	cag Gln 195	ggg Gly	agt Ser	ttc Phe	cgc Arg	tgc Cys 200	ctg Leu	cgc Arg	ttt Phe	gat Asp	tgt Cys 205	cca Pro	ccc Pro	aac Asn	624
tat Tyr 210	gtc Val	cgt Arg	gtc Val	tca Ser	caa Gln	acg Thr 215	aag Lys	tgc Cys	gag Glu	cgc Arg	acc Thr 220	aca Thr	tgc Cys	cag Gln	gat Asp	672
atc Ile 225	acg Thr	gaa Glu	tgt Cys	caa Gln	acc Thr 230	tca Ser	cca Pro	gct Ala	cgc Arg	atc Ile 235	acg Thr	cac His	tac Tyr	cag Gln	ctc Leu 240	720
aat Asn	ttc Phe	cag Gln	aca Thr	ggc Gly 245	cta Leu	ctg Leu	gta Val	cct Pro	gca Ala 250	cat His	atc Ile	ttc Phe	cgc Arg	atc Ile 255	ggc Gly	768
cct Pro	gct Ala	ccc Pro	gcc Ala 260	ttt Phe	gct Ala	ggg Gly	gac Asp	acc Thr 265	atc Ile	tcc Ser	ctg Leu	acc Thr	atc Ile 270	acg Thr	aag Lys	816
ggc Gly	aat Asn	gag Glu 275	gag Glu	ggc Gly	tac Tyr	ttc Phe	gtc Val 280	aca Thr	cgc Arg	aga Arg	ctc Leu	aat Asn 285	gcc Ala	tac Tyr	act Thr	864
ggt Gly 290	gtg Val	gta Val	tcc Ser	ctg Leu	cag Gln	cgg Arg 295	tct Ser	gtt Val	ctg Leu	gag Glu	ccg Pro 300	cgg Arg	gac Asp	ttt Phe	gcc Ala	912



Conseiller.ST25

cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc 960  
 Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
 305 310 315 320

ctg gcc aag atg tac atc ttc ttc acc act ttt gcc cca tgaggtgaca 1009  
 Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro  
 325 330

tgtcaggcaa tccctccagg tgatgcctgg gcggtgggca gctgcgccac tcctaagtgg 1069  
 ctttttgctg tgactctgta acttaactta atcatgctga gctggttggg cttgagtctc 1129  
 taccctagag ggagggagat gcaccccagc aggcactgag tacaggccag ggtcacccga 1189  
 ggctagatgg tgacctgcaa actggaaaca gccatagggg gcttctgaac tccactcctc 1249  
 aactatggct acagctgaca ttccattcct tcatccactg tgttcctcaa ttaaaaaaaaa 1309  
 aaatcagctg tgcattgtag cacagacctt taatcctagc actggggagg cagaggtagg 1369  
 tagatctctg agttccaggc cagcctgggc tacactggga gttctaacca gccagagcta 1429  
 catagagaga ccctatctca acaaggaaaa aacgaaagaa atctctgtga gttccaggcc 1489  
 agcctgggtc acgctgggag ttctaaccag ccagagctac atagagagat cctatctcaa 1549  
 caaggaaaaa tgaaagaaat ctttttaaaa ggtttttttt tttgctgttg ttgtttaatg 1609  
 ataagagtag cacatataca ttattaaaaa tgatcaaata gcacagaaag gtta 1663

<210> 33

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine fibulin 2 c-term fragment

<400> 33

Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His  
 1 5 10 15

Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg  
 20 25 30

Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys  
 35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His  
 50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly  
 65 70 75 80

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Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys  
85 90 95

Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr  
100 105 110

Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr  
115 120 125

Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr  
130 135 140

Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu  
145 150 155 160

Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp  
165 170 175

Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His  
180 185 190

Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn  
195 200 205

Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp  
210 215 220

Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu  
225 230 235 240

Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly  
245 250 255

Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys  
260 265 270

Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr  
275 280 285

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala  
290 295 300

Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
305 310 315 320

Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro

325

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330

<210> 34

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine N-terminal signal sequence

<400> 34

Ala Val Ala Glu Thr Pro Asp Phe Cys Pro Pro Pro Ser Leu Arg  
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<210> 35

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Human N-terminal signal sequence

<400> 35

Ser Gln Pro Ser Arg Gln Ser Arg Gly Pro Arg Gly Cys Arg Gly Pro  
1 5 10 15

Asn Pro Arg